

Search History for 10/694,779

(FILE 'HOME' ENTERED AT 14:23:31 ON 08 JAN 2007)

FILE 'REGISTRY' ENTERED AT 14:24:11 ON 08 JAN 2007

E "AMMONIAGENES"/CN 25

E "FOF1-ATPASE"/CN 25

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
14:25:07 ON 08 JAN 2007

L1 4 S AMMONIAGENES AND ATPASE

L2 3 DUP REM L1 (1 DUPLICATE REMOVED)

FILE 'STNGUIDE' ENTERED AT 14:26:38 ON 08 JAN 2007

L3 0 S AMMONIAGENES AND "PROTON PUMP"

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
14:49:42 ON 08 JAN 2007

L4 0 S AMMONIAGENES AND "PROTON PUMP"

L5 1954 S AMMONIAGENES

L6 2 S L5 AND FOF1?

L7 2 DUP REM L6 (0 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 14:50:45 ON 08 JAN 2007

L8 0 S L5 AND FOF1?

FILE 'REGISTRY' ENTERED AT 14:57:09 ON 08 JAN 2007

E "ATP SYNTHASE"/CN 25

L9 1 S E3

FILE 'MEDLINE, AGRICOLA, CAPLUS, BIOSIS, EMBASE, WPIDS' ENTERED AT
15:00:08 ON 08 JAN 2007

L10 10673 S L9

L11 0 S L5 AND L10

L12 0 S L5 AND 3.6.3.14

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Search

Most Recent Queries

Time Result

<u>#23</u>	Search #22 AND (corynebacterium OR coryneform OR ammoniagenes)	14:57:09	<u>0</u>
<u>#22</u>	Search "Proton-Translocating ATPases"[MeSH]	14:56:43	<u>8984</u>
<u>#19</u>	Search #12 AND corynebacterium	14:14:52	<u>14</u>
<u>#18</u>	Search #12 AND coryneform	14:14:45	<u>0</u>
<u>#17</u>	Search #12 AND ammoniagenes	14:14:37	<u>0</u>
<u>#16</u>	Search #15 AND ammoniagenes	14:14:23	<u>0</u>
<u>#15</u>	Related Articles for PubMed (Select 6241036)	14:14:11	<u>232</u>
<u>#14</u>	Search #13 AND 1984	14:14:05	<u>81</u>
<u>#13</u>	Search #12 AND coli	14:11:47	<u>2099</u>
<u>#12</u>	Search "Proton Pumps"[MeSH]	14:11:35	<u>31149</u>
<u>#10</u>	Search ammoniagenes and genomic	14:07:15	<u>15</u>
<u>#9</u>	Search ammoniagenes	14:06:42	<u>142</u>
<u>#8</u>	Search "Actinomycetales"[MeSH]	14:05:33	<u>88269</u>
<u>#2</u>	Search "Glucokinase"[MeSH]	09:04:27	<u>1987</u>
<u>#3</u>	Search #2 AND crystal	09:04:26	<u>12</u>

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Dec 18 2006 06:34:27

IUBMB Enzyme Nomenclature

EC 3.6.3.14

Accepted name: H⁺-transporting two-sector ATPase

Reaction: ATP + H₂O + H⁺_{in} = ADP + phosphate + H⁺_{out}

Glossary: F_o the "o" refers to oligomycin. F₀ is incorrect.

Other names: ATP synthase; F₁-ATPase; F₀F₁-ATPase; H⁺-transporting ATPase; mitochondrial ATPase; coupling factors (F₀, F₁ and CF₁); chloroplast ATPase; bacterial Ca²⁺/Mg²⁺ ATPase

Systematic name: ATP phosphohydrolase (H⁺-transporting)

Comments: A multisubunit non-phosphorylated ATPase that is involved in the transport of ions. Large enzymes of mitochondria, chloroplasts and bacteria with a membrane sector (F_{ox}, V_o, A_o) and a cytoplasmic-compartment sector (F₁, V₁, A₁). The F-type enzymes of the inner mitochondrial and thylakoid membranes act as ATP synthases. All of the enzymes included here operate in a rotational mode, where the extramembrane sector (containing 3 α- and 3 β-subunits) is connected via the δ-subunit to the membrane sector by several smaller subunits. Within this complex, the γ- and ε-subunits, as well as the 9-12 c subunits rotate by consecutive 120° angles and perform parts of ATP synthesis. This movement is driven by the H⁺ electrochemical potential gradient. The V-type (in vacuoles and clathrin-coated vesicles) and A-type (archebacterial) enzymes have a similar structure but, under physiological conditions, they pump H⁺ rather than synthesize ATP.

Links to other databases: [BRENDA](#), [EXPASY](#), [KEGG](#), [ERGO](#), [PDB](#), CAS registry number:

References:

1. Boyer, P.D. The binding change mechanism for ATP synthase - some probabilities and possibilities. *Biochim. Biophys. Acta* 1140 (1993) 215-250. [Medline UI: [93112640](#)]
2. Abrahams, J.P., Leslie, A.G.W., Lutter, R. and Walker, J.F. Structure at 2.8 Å resolution of F₁-ATPase from bovine heart mitochondria. *Nature* 375 (1994) 621-628. [Medline UI: [94344236](#)]
3. Blair, A., Ngo, L., Park, J., Paulsen, I.T. and Saier, M.H., Jr. Phylogenetic analyses of the homologous transmembrane channel-forming proteins of the F₀F₁-ATPases of bacteria, chloroplasts and mitochondria. *Microbiology* 142 (1996) 17-32. [Medline UI: [96146047](#)]
4. Noji, H., Yasuda, R., Yoshida, M. and Kinosita, K., Jr. Direct observation of the rotation of F₁-ATPase. *Nature* 386 (1997) 299-302. [Medline UI: [97222141](#)]

[EC 3.6.3.14 created 1984 as EC 3.6.1.34, transferred 2000 to EC 3.6.3.14]

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☒ 1: Proton-Translocating ATPases

Multisubunit enzymes that reversibly synthesize ADENOSINE TRIPHOSPHATE. They are coupled to the transport of protons across a membrane.

Year introduced: 2002(1983)

Subheadings: This list includes those paired at least once with this heading in MEDLINE and may not reflect current rules for allowable combinations.

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Registry Number: EC 3.6.3.14

Entry Terms:

- H(+)-ATPase
- H+-Translocating ATPase
- ATPase, H+-Translocating
- H+ Translocating ATPase
- Proton-Translocating ATPase
- ATPase, Proton-Translocating
- Proton Translocating ATPase
- H(+)ATPase Complex
- ATPase, F(1)F(0)
- ATPase, FOF1

- F(0)F(1)-ATP Synthase
- ATPase, H(+)
- Proton-Translocating ATPase Complexes
- ATPase Complexes, Proton-Translocating
- Complexes, Proton-Translocating ATPase
- Proton Translocating ATPase Complexes
- H(+)-Transporting ATPase
- F1F0 ATPase Complex
- ATP Dependent Proton Translocase
- H+ ATPase
- ATPase, H+
- F0F1 ATPase
- F(1)F(0)-ATPase
- Proton-Translocating ATPase Complex
- ATPase Complex, Proton-Translocating
- Proton Translocating ATPase Complex
- H+ Transporting ATP Synthase
- H(+)-Transporting ATP Synthase
- Adenosine Triphosphatase Complex
- Complex, Adenosine Triphosphatase
- Triphosphatase Complex, Adenosine
- Proton-Translocating ATPase, F1 Sector
- Proton Translocating ATPase, F1 Sector
- F1-ATPase
- ATPase, F1
- F1 ATPase
- Adenosinetriphosphatase F1
- F-1-ATPase
- F 1 ATPase
- H(+)-Transporting ATP Synthase, Acyl-Phosphate-Linked
- Proton-Translocating ATPase, F0 Sector
- Proton Translocating ATPase, F0 Sector
- ATPase, F0
- F0 ATPase
- F-0-ATPase
- F 0 ATPase

Previous Indexing:

- Adenosine Triphosphatase (1966-1982)

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Steadman, David

From: Steadman, David
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Please search the following sequence in commercial and interference databases:

STANDARD search of SEQ ID NO:9 against nucleic acid databases.

Thank you very much.

David J. Steadman, Ph.D.
Primary Examiner
Art Unit 1656
Protein Crystallography and Recombinant Enzymes
Office: Remsen 2B05
Mailbox: Remsen 3C70
Phone: (571) 272-0942